



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 21, 2024 – 01:09 AM EDT

PDB ID : 2L0Z  
Title : Solution structure of a zinc-binding domain from the Junin virus envelope glycoprotein  
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Deposited on : 2010-07-21

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We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
wwPDB-RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
wwPDB-ShiftChecker : v1.2  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

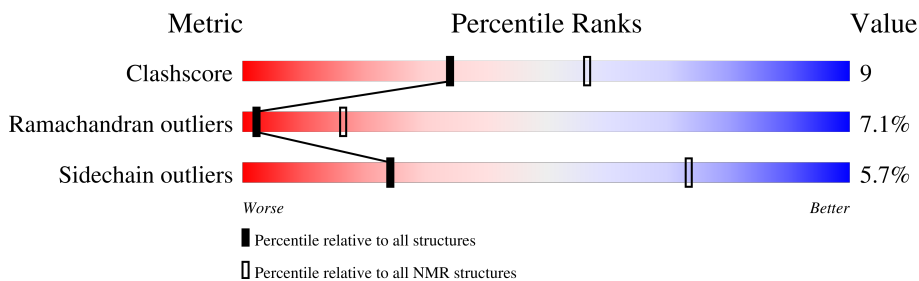
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	42	

## 2 Ensemble composition and analysis

This entry contains 21 models. Model 21 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:446-A:485 (40)	1.01	21

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 6, 7, 10, 12, 13, 14, 15, 18, 19, 20, 21
2	8, 16, 17
Single-model clusters	5; 9; 11

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 670 atoms, of which 335 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called glycoprotein G2.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	42	668	206	335	73	51	3	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	444	ACE	-	acetylation	UNP P26313

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

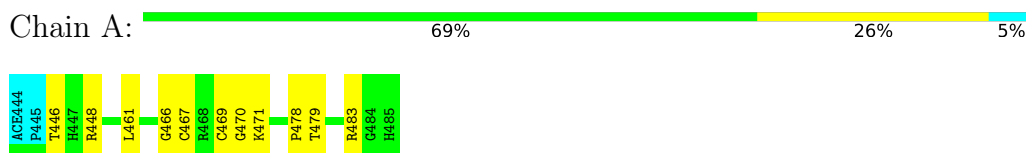
Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	2	2	2

## 4 Residue-property plots

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: glycoprotein G2

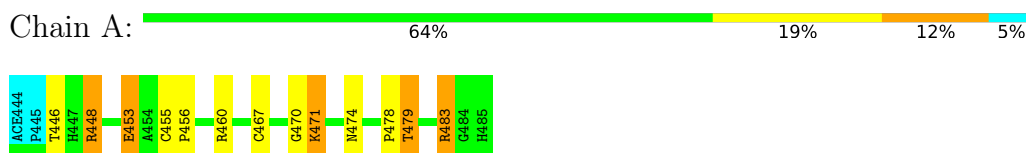


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

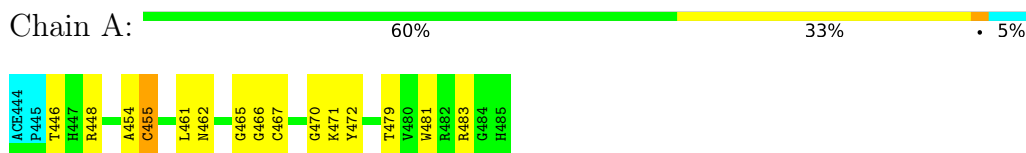
#### 4.2.1 Score per residue for model 1

- Molecule 1: glycoprotein G2



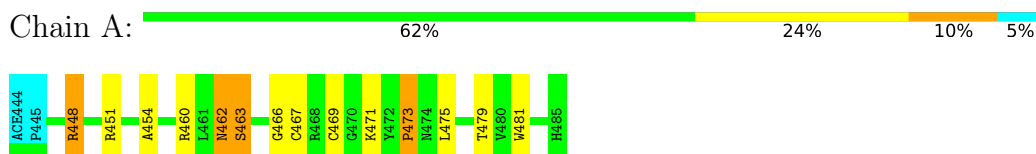
#### 4.2.2 Score per residue for model 2

- Molecule 1: glycoprotein G2



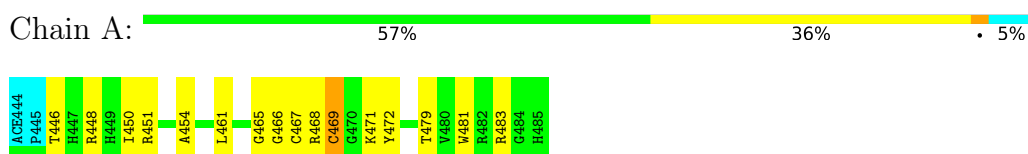
### 4.2.3 Score per residue for model 3

- Molecule 1: glycoprotein G2



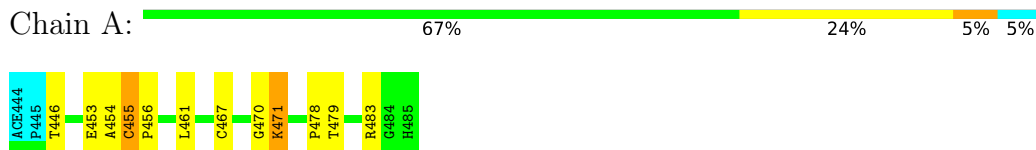
### 4.2.4 Score per residue for model 4

- Molecule 1: glycoprotein G2



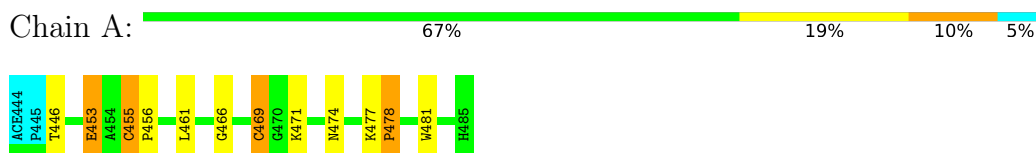
### 4.2.5 Score per residue for model 5

- Molecule 1: glycoprotein G2



### 4.2.6 Score per residue for model 6

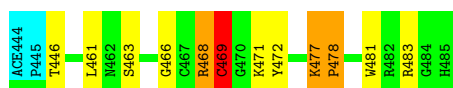
- Molecule 1: glycoprotein G2



### 4.2.7 Score per residue for model 7

- Molecule 1: glycoprotein G2





#### 4.2.8 Score per residue for model 8

- Molecule 1: glycoprotein G2

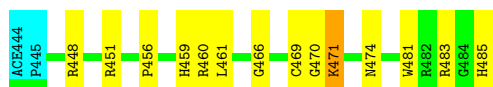
Chain A: 79% 14% 5%



#### 4.2.9 Score per residue for model 9

- Molecule 1: glycoprotein G2

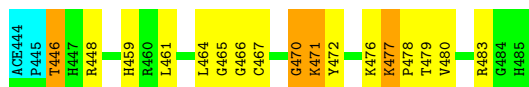
Chain A: 62% 31% 5%



#### 4.2.10 Score per residue for model 10

- Molecule 1: glycoprotein G2

Chain A: 55% 31% 10% 5%



#### 4.2.11 Score per residue for model 11

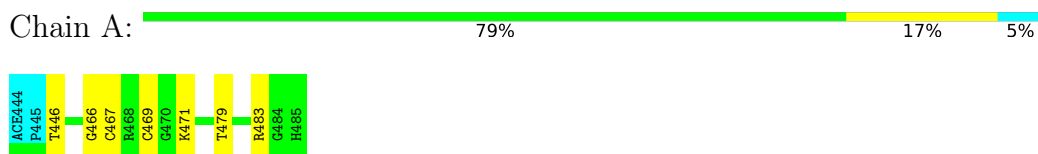
- Molecule 1: glycoprotein G2

Chain A: 67% 29% 5%



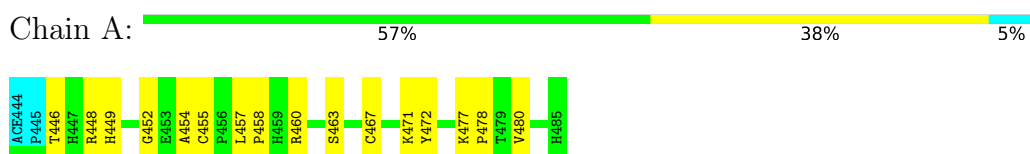
#### 4.2.12 Score per residue for model 12

- Molecule 1: glycoprotein G2



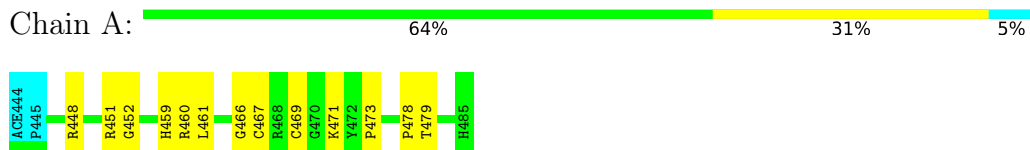
#### 4.2.13 Score per residue for model 13

- Molecule 1: glycoprotein G2



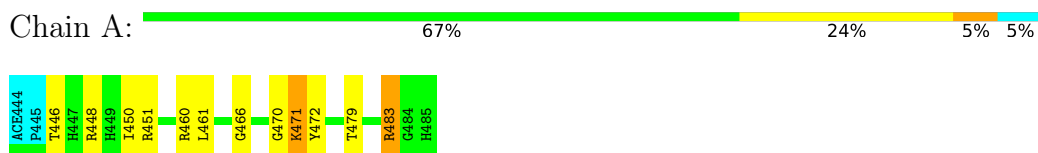
#### 4.2.14 Score per residue for model 14

- Molecule 1: glycoprotein G2



#### 4.2.15 Score per residue for model 15

- Molecule 1: glycoprotein G2

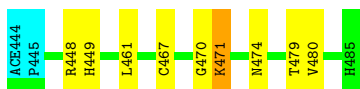


#### 4.2.16 Score per residue for model 16

- Molecule 1: glycoprotein G2



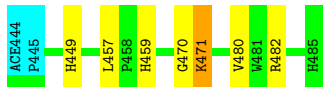




#### 4.2.17 Score per residue for model 17

- Molecule 1: glycoprotein G2

Chain A: 79% 14% 5%



#### 4.2.18 Score per residue for model 18

- Molecule 1: glycoprotein G2

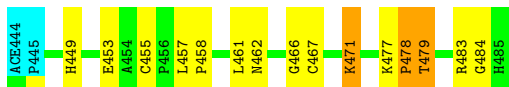
Chain A: 57% 38% 5%



#### 4.2.19 Score per residue for model 19

- Molecule 1: glycoprotein G2

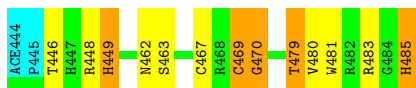
Chain A: 60% 29% 7% 5%



#### 4.2.20 Score per residue for model 20

- Molecule 1: glycoprotein G2

Chain A: 64% 19% 12% 5%



#### 4.2.21 Score per residue for model 21 (medoid)

- Molecule 1: glycoprotein G2

Chain A:  64% 29% • 5%



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *molecular dynamics*.

Of the 56 calculated structures, 21 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
ARIA	structure solution	1.2
ARIA	refinement	1.2

No chemical shift data was provided.

## 6 Model quality i

### 6.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ACE, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.51±0.08	1±1/333 ( 0.2± 0.2%)	0.54±0.07	0±1/446 ( 0.1± 0.1%)
All	All	0.52	13/6993 ( 0.2%)	0.55	6/9366 ( 0.1%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	451	ARG	CD-NE	6.49	1.57	1.46	14	1
1	A	485	HIS	CB-CG	-6.08	1.39	1.50	20	1
1	A	472	TYR	CD2-CE2	6.04	1.48	1.39	21	1
1	A	481	TRP	CZ3-CH2	5.82	1.49	1.40	7	1
1	A	465	GLY	C-O	-5.60	1.14	1.23	4	1
1	A	454	ALA	N-CA	-5.48	1.35	1.46	18	1
1	A	478	PRO	N-CD	-5.43	1.40	1.47	14	1
1	A	448	ARG	C-N	-5.37	1.21	1.34	3	1
1	A	468	ARG	CZ-NH1	5.30	1.40	1.33	11	1
1	A	466	GLY	C-O	5.19	1.31	1.23	12	1
1	A	467	CYS	CB-SG	-5.17	1.73	1.81	18	1
1	A	481	TRP	CZ2-CH2	5.15	1.47	1.37	6	1
1	A	480	VAL	C-O	-5.10	1.13	1.23	10	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	468	ARG	NE-CZ-NH2	8.43	124.52	120.30	11	1
1	A	472	TYR	CG-CD2-CE2	-7.88	115.00	121.30	21	1
1	A	472	TYR	CB-CG-CD2	-6.94	116.84	121.00	21	1
1	A	468	ARG	NE-CZ-NH1	-5.57	117.52	120.30	11	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	481	TRP	CZ3-CH2-CZ2	-5.28	115.27	121.60	6	1
1	A	448	ARG	NE-CZ-NH2	-5.14	117.73	120.30	1	1

There are no chirality outliers.

There are no planarity outliers.

## 6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	323	325	325	6±2
All	All	6825	6825	6824	121

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:446:THR:HG22	1:A:483:ARG:HB2	0.75	1.57	5	4
1:A:448:ARG:HB3	1:A:479:THR:HB	0.73	1.60	15	3
1:A:467:CYS:SG	1:A:471:LYS:HB3	0.73	2.23	11	9
1:A:449:HIS:HB2	1:A:480:VAL:HB	0.71	1.59	16	6
1:A:446:THR:HG22	1:A:483:ARG:HG2	0.67	1.65	15	1
1:A:448:ARG:HB2	1:A:461:LEU:HB2	0.62	1.71	14	2
1:A:470:GLY:O	1:A:471:LYS:HB2	0.59	1.97	5	7
1:A:461:LEU:HA	1:A:466:GLY:O	0.59	1.98	6	9
1:A:468:ARG:O	1:A:469:CYS:HB3	0.57	1.99	7	1
1:A:460:ARG:O	1:A:467:CYS:HA	0.56	2.00	3	3
1:A:464:LEU:O	1:A:476:LYS:HA	0.54	2.01	10	1
1:A:446:THR:HG23	1:A:483:ARG:HB2	0.54	1.78	2	3
1:A:456:PRO:HB3	1:A:461:LEU:HD21	0.54	1.77	6	1
1:A:448:ARG:NH1	1:A:463:SER:HA	0.54	2.17	13	2
1:A:457:LEU:HB3	1:A:458:PRO:HA	0.53	1.81	18	3
1:A:459:HIS:HB3	1:A:467:CYS:SG	0.52	2.44	10	1
1:A:448:ARG:HG2	1:A:481:TRP:CZ3	0.51	2.40	9	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:466:GLY:HA2	1:A:472:TYR:HB2	0.51	1.82	2	2
1:A:461:LEU:HG	1:A:466:GLY:N	0.51	2.21	10	1
1:A:451:ARG:HD3	1:A:478:PRO:HG2	0.51	1.81	18	1
1:A:456:PRO:HB2	1:A:461:LEU:HD21	0.51	1.83	5	1
1:A:448:ARG:CD	1:A:479:THR:HB	0.49	2.36	1	1
1:A:457:LEU:HA	1:A:459:HIS:N	0.49	2.21	8	2
1:A:469:CYS:SG	1:A:471:LYS:HB2	0.49	2.47	6	1
1:A:477:LYS:HB3	1:A:478:PRO:HD2	0.49	1.85	10	3
1:A:456:PRO:CB	1:A:461:LEU:HG	0.48	2.38	9	1
1:A:448:ARG:HD3	1:A:479:THR:HG21	0.48	1.84	10	1
1:A:456:PRO:CB	1:A:461:LEU:HD21	0.48	2.38	6	2
1:A:448:ARG:HD3	1:A:479:THR:HB	0.48	1.86	1	1
1:A:450:ILE:HG13	1:A:461:LEU:HD21	0.47	1.87	4	1
1:A:449:HIS:CB	1:A:480:VAL:HB	0.47	2.36	16	1
1:A:462:ASN:OD1	1:A:467:CYS:HA	0.47	2.10	20	1
1:A:461:LEU:HB3	1:A:465:GLY:HA2	0.46	1.87	2	1
1:A:449:HIS:CE1	1:A:455:CYS:HA	0.46	2.45	19	1
1:A:449:HIS:CE1	1:A:482:ARG:HG3	0.45	2.46	17	1
1:A:462:ASN:HD22	1:A:463:SER:N	0.45	2.10	3	1
1:A:446:THR:CG2	1:A:483:ARG:HB2	0.45	2.40	11	1
1:A:483:ARG:HG3	1:A:484:GLY:N	0.44	2.26	19	1
1:A:446:THR:CG2	1:A:483:ARG:HB3	0.44	2.43	12	1
1:A:446:THR:HA	1:A:483:ARG:CG	0.44	2.42	1	1
1:A:471:LYS:HD2	1:A:472:TYR:CE2	0.43	2.49	4	3
1:A:470:GLY:O	1:A:471:LYS:CB	0.43	2.65	10	1
1:A:453:GLU:HG3	1:A:456:PRO:HG3	0.43	1.90	1	1
1:A:476:LYS:HG2	1:A:476:LYS:O	0.43	2.13	21	1
1:A:473:PRO:HD2	1:A:475:LEU:HG	0.43	1.89	3	1
1:A:477:LYS:HB2	1:A:478:PRO:HD2	0.43	1.89	19	2
1:A:454:ALA:O	1:A:455:CYS:HB2	0.43	2.14	5	3
1:A:446:THR:HA	1:A:483:ARG:HB2	0.43	1.91	4	1
1:A:450:ILE:O	1:A:451:ARG:HG2	0.43	2.13	15	1
1:A:468:ARG:O	1:A:469:CYS:CB	0.42	2.67	4	1
1:A:446:THR:HA	1:A:483:ARG:HG3	0.42	1.92	1	1
1:A:466:GLY:HA2	1:A:472:TYR:CB	0.42	2.45	2	1
1:A:459:HIS:CE1	1:A:471:LYS:HD2	0.42	2.50	9	1
1:A:477:LYS:HG3	1:A:478:PRO:HD2	0.42	1.90	6	1
1:A:459:HIS:HB3	1:A:467:CYS:CB	0.41	2.45	14	2
1:A:469:CYS:SG	1:A:470:GLY:N	0.41	2.93	20	1
1:A:449:HIS:ND1	1:A:482:ARG:HG3	0.41	2.30	17	1
1:A:446:THR:OG1	1:A:481:TRP:HB3	0.41	2.15	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:449:HIS:O	1:A:479:THR:HG22	0.41	2.15	19	1
1:A:471:LYS:HD3	1:A:471:LYS:C	0.41	2.35	4	1
1:A:471:LYS:HD3	1:A:472:TYR:CE2	0.41	2.50	10	1
1:A:471:LYS:HD2	1:A:472:TYR:CE1	0.41	2.51	15	1
1:A:453:GLU:HG2	1:A:455:CYS:N	0.40	2.30	6	1
1:A:448:ARG:HB3	1:A:479:THR:CB	0.40	2.41	15	1
1:A:453:GLU:HG2	1:A:455:CYS:H	0.40	1.76	6	1
1:A:466:GLY:HA3	1:A:473:PRO:O	0.40	2.17	3	1

## 6.3 Torsion angles [i](#)

### 6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	39/42 (93%)	30±3 (77±8%)	6±2 (16±5%)	3±1 (7±4%)	2	16
All	All	819/882 (93%)	634 (77%)	127 (16%)	58 (7%)	2	16

All 19 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	471	LYS	13
1	A	470	GLY	5
1	A	478	PRO	5
1	A	455	CYS	4
1	A	469	CYS	4
1	A	446	THR	4
1	A	451	ARG	3
1	A	463	SER	3
1	A	460	ARG	3
1	A	454	ALA	2
1	A	473	PRO	2
1	A	483	ARG	2
1	A	452	GLY	2
1	A	462	ASN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	468	ARG	1
1	A	465	GLY	1
1	A	477	LYS	1
1	A	474	ASN	1
1	A	476	LYS	1

### 6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	34/35 (97%)	32±1 (94±4%)	2±1 (6±4%)	24	73
All	All	714/735 (97%)	673 (94%)	41 (6%)	24	73

All 13 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	479	THR	11
1	A	469	CYS	8
1	A	453	GLU	4
1	A	474	ASN	3
1	A	483	ARG	3
1	A	462	ASN	3
1	A	446	THR	2
1	A	485	HIS	2
1	A	460	ARG	1
1	A	477	LYS	1
1	A	468	ARG	1
1	A	449	HIS	1
1	A	480	VAL	1

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.



## 6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided